

Jordan

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/500/84/A
Source: PCF
Date Processed by STIC: 3-4-05

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PCT

RAW SEQUENCE LISTING

DATE: 03/04/2005

PATENT APPLICATION: US/10/500,841A

TIME: 12:13:40

Input Set : A:\034100-003.txt

Output Set: N:\CRF4\03042005\J500841A.raw

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4 <110> APPLICANT: Taniguchi, Naoyuki
5     Miyoshi, Eiji
6     Saito, Takeshi
8 <120> TITLE OF INVENTION: Glycosyltransferase GnT-V Having Neovascularization Action
10 <130> FILE REFERENCE: 034100-003
12 <140> CURRENT APPLICATION NUMBER: US 10/500,841A
13 <141> CURRENT FILING DATE: 2004-07-07
15 <150> PRIOR APPLICATION NUMBER: PCT/JP02/13879
16 <151> PRIOR FILING DATE: 2002-12-27
18 <150> PRIOR APPLICATION NUMBER: JP 2002-2056
19 <151> PRIOR FILING DATE: 2002-01-09
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 5
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
31 Thr Pro Trp Gly Lys
32 1      5
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 6
36 <212> TYPE: PRT
37 <213> ORGANISM: Homo sapiens
39 <400> SEQUENCE: 2
40 Asn Ile Pro Ser Tyr Val
41 1      5
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 17
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
49 <400> SEQUENCE: 3
50 Val Leu Asp Ser Phe Gly Thr Glu Pro Glu Phe Asn His Ala Asn Tyr
51 1      5          10          15
52 Ala
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 6
58 <212> TYPE: PRT
59 <213> ORGANISM: Homo sapiens
61 <400> SEQUENCE: 4
62 Asp Leu Gln Phe Leu Leu
63 1      5
66 <210> SEQ ID NO: 5

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67 <211> LENGTH: 7
68 <212> TYPE: PRT
69 <213> ORGANISM: Homo sapiens
71 <400> SEQUENCE: 5
72 Asn Thr Asp Phe Phe Ile Gly
73 1 5
76 <210> SEQ ID NO: 6
77 <211> LENGTH: 2095
78 <212> TYPE: DNA
79 <213> ORGANISM: Homo sapiens
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (156)...(2095)
85 <400> SEQUENCE: 6
86 ccggctgaag catcagaatg gaagtgagga aaggcaacca gctgacacag gagccagagt 60
87 gagaccagca gactctcaca ctcaacctac accatgaatt tgtgtctatc ttctacgcgt 120
88 taagagccaa ggacaggtga agttgccaga gagca atg gct ctc ttc act ccg 173
89 Met Ala Leu Phe Thr Pro
90 1 5
92 tgg aag ttg tcc tct cag aag ctg ggc ttt ttc ctg gtg act ttt ggc 221
93 Trp Lys Leu Ser Ser Gln Lys Leu Gly Phe Phe Leu Val Thr Phe Gly
94 10 15 20
96 ttc att tgg ggt atg atg ctt ctg cac ttt acc atc cag cag cga act 269
97 Phe Ile Trp Gly Met Met Leu Leu His Phe Thr Ile Gln Gln Arg Thr
98 25 30 35
100 cag cct gaa agc agc tcc atg ctg cgc gag cag atc ctg gac ctc agc 317
101 Gln Pro Glu Ser Ser Ser Met Leu Arg Glu Gln Ile Leu Asp Leu Ser
102 40 45 50
104 aaa agg tac atc aag gca ctg gca gaa gaa aac agg aat gtg gtg gat 365
105 Lys Arg Tyr Ile Lys Ala Leu Ala Glu Glu Asn Arg Asn Val Val Asp
106 55 60 65 70
108 ggg cca tac gct gga gtc atg aca gct tat gat ctg aag aaa acc ctt 413
109 Gly Pro Tyr Ala Gly Val Met Thr Ala Tyr Asp Leu Lys Lys Thr Leu
110 75 80 85
112 gct gtg tta tta gat aac att ttg cag cgc att ggc aag ttg gag tcg 461
113 Ala Val Leu Leu Asp Asn Ile Leu Gln Arg Ile Gly Lys Leu Glu Ser
114 90 95 100
116 aag gtg gac aat ctt gtt gtc aat ggc acc gga aca aac tca acc aac 509
117 Lys Val Asp Asn Leu Val Val Asn Gly Thr Gly Thr Asn Ser Thr Asn
118 105 110 115
120 tcc act aca gct gtt ccc agc ttg gtt gca ctt gag aaa att aat gtg 557
121 Ser Thr Thr Ala Val Pro Ser Leu Val Ala Leu Glu Lys Ile Asn Val
122 120 125 130
124 gca gat atc att aac gga gct caa gaa aaa tgt gta ttg cct cct atg 605
125 Ala Asp Ile Ile Asn Gly Ala Gln Glu Lys Cys Val Leu Pro Pro Met
126 135 140 145 150
128 gac ggc tac cct cac tgt gag gga aag atc aag tgg atg aaa gac atg 653
129 Asp Gly Tyr Pro His Cys Glu Gly Lys Ile Lys Trp Met Lys Asp Met
130 155 160 165

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DATE: 03/04/2005

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Input Set : A:\034100-003.txt

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 132 | tgg | cgt | tca | gat | ccc | tgc | tac | gca | gac | tat | gga | gtg | gat | gga | tcc | acc | 701 |
| 133 | Trp | Arg | Ser | Asp | Pro | Cys | Tyr | Ala | Asp | Tyr | Gly | Val | Asp | Gly | Ser | Thr | |
| 134 | | | | 170 | | | | | 175 | | | | | 180 | | | |
| 136 | tgc | tct | ttt | ttt | att | tac | ctc | agt | gag | gtt | gaa | aat | tgg | tgt | cct | cat | 749 |
| 137 | Cys | Ser | Phe | Phe | Ile | Tyr | Leu | Ser | Glu | Val | Glu | Asn | Trp | Cys | Pro | His | |
| 138 | | | 185 | | | | | 190 | | | | | 195 | | | | |
| 140 | tta | cct | tgg | aga | gca | aaa | aat | ccc | tac | gaa | gaa | gct | gat | cat | aat | tca | 797 |
| 141 | Leu | Pro | Trp | Arg | Ala | Lys | Asn | Pro | Tyr | Glu | Glu | Ala | Asp | His | Asn | Ser | |
| 142 | | 200 | | | | | 205 | | | | | 210 | | | | | |
| 144 | ttg | gcg | gaa | att | cgt | aca | gat | ttt | aat | att | ctc | tac | agt | atg | atg | aaa | 845 |
| 145 | Leu | Ala | Glu | Ile | Arg | Thr | Asp | Phe | Asn | Ile | Leu | Tyr | Ser | Met | Met | Lys | |
| 146 | 215 | | | | 220 | | | | | 225 | | | | | 230 | | |
| 148 | aag | cat | gaa | gaa | ttc | cgg | tgg | atg | aga | cta | cgg | atc | cgg | cga | atg | gct | 893 |
| 149 | Lys | His | Glu | Glu | Phe | Arg | Trp | Met | Arg | Leu | Arg | Ile | Arg | Arg | Met | Ala | |
| 150 | | | | 235 | | | | | 240 | | | | | 245 | | | |
| 152 | gac | gca | tgg | atc | caa | gca | atc | aag | tcc | ctg | gca | gaa | aag | cag | aac | ctt | 941 |
| 153 | Asp | Ala | Trp | Ile | Gln | Ala | Ile | Lys | Ser | Leu | Ala | Glu | Lys | Gln | Asn | Leu | |
| 154 | | | 250 | | | | | 255 | | | | | 260 | | | | |
| 156 | gaa | aag | aga | aag | cgg | aag | aaa | gtc | ctc | gtt | cac | ctg | gga | ctc | ctg | acc | 989 |
| 157 | Glu | Lys | Arg | Lys | Arg | Lys | Lys | Val | Leu | Val | His | Leu | Gly | Leu | Leu | Thr | |
| 158 | | 265 | | | | | 270 | | | | | 275 | | | | | |
| 160 | aag | gaa | tct | gga | ttt | aag | att | gca | gag | aca | gct | ttc | agt | ggg | ggc | cct | 1037 |
| 161 | Lys | Glu | Ser | Gly | Phe | Lys | Ile | Ala | Glu | Thr | Ala | Phe | Ser | Gly | Gly | Pro | |
| 162 | | 280 | | | | 285 | | | | | 290 | | | | | | |
| 164 | ctt | ggg | gaa | tta | gtt | caa | tgg | agt | gat | tta | att | aca | tct | ctg | tac | tta | 1085 |
| 165 | Leu | Gly | Glu | Leu | Val | Gln | Trp | Ser | Asp | Leu | Ile | Thr | Ser | Leu | Tyr | Leu | |
| 166 | 295 | | | | 300 | | | | | 305 | | | | | 310 | | |
| 168 | ctg | ggc | cat | gac | att | agg | att | tca | gct | tca | ctg | gct | gag | ctc | aag | gaa | 1133 |
| 169 | Leu | Gly | His | Asp | Ile | Arg | Ile | Ser | Ala | Ser | Leu | Ala | Glu | Leu | Lys | Glu | |
| 170 | | | | 315 | | | | | 320 | | | | | | 325 | | |
| 172 | atc | atg | aag | aag | gtt | gta | gga | aac | cga | tct | ggc | tgc | cca | act | gta | gga | 1181 |
| 173 | Ile | Met | Lys | Lys | Val | Val | Gly | Asn | Arg | Ser | Gly | Cys | Pro | Thr | Val | Gly | |
| 174 | | | 330 | | | | | 335 | | | | | 340 | | | | |
| 176 | gac | aga | att | gtt | gag | ctc | att | tac | att | gat | att | gta | gga | ctt | gct | caa | 1229 |
| 177 | Asp | Arg | Ile | Val | Glu | Leu | Ile | Tyr | Ile | Asp | Ile | Val | Gly | Leu | Ala | Gln | |
| 178 | | 345 | | | | | 350 | | | | | 355 | | | | | |
| 180 | ttc | aag | aaa | act | ctt | gga | cca | tcc | tgg | gtt | cat | tac | cag | tgc | atg | ctc | 1277 |
| 181 | Phe | Lys | Lys | Thr | Leu | Gly | Pro | Ser | Trp | Val | His | Tyr | Gln | Cys | Met | Leu | |
| 182 | | 360 | | | | 365 | | | | | 370 | | | | | | |
| 184 | cga | gtc | ctt | gat | tca | ttt | ggg | act | gaa | ccc | gaa | ttt | aat | cat | gca | aat | 1325 |
| 185 | Arg | Val | Leu | Asp | Ser | Phe | Gly | Thr | Glu | Pro | Glu | Phe | Asn | His | Ala | Asn | |
| 186 | 375 | | | | 380 | | | | | 385 | | | | 390 | | | |
| 188 | tat | gcc | caa | tcg | aaa | ggc | cac | aag | acc | cct | tgg | gga | aaa | tgg | aat | ctg | 1373 |
| 189 | Tyr | Ala | Gln | Ser | Lys | Gly | His | Lys | Thr | Pro | Trp | Gly | Lys | Trp | Asn | Leu | |
| 190 | | | | 395 | | | | 400 | | | | | 405 | | | | |
| 192 | aac | cct | cag | cag | ttt | tat | acc | atg | ttc | cct | cat | acc | cca | gac | aac | agc | 1421 |
| 193 | Asn | Pro | Gln | Gln | Phe | Tyr | Thr | Met | Phe | Pro | His | Thr | Pro | Asp | Asn | Ser | |
| 194 | | | 410 | | | | | 415 | | | | | 420 | | | | |
| 196 | ttt | ctg | ggg | ttt | gtg | gtt | gag | cag | cac | ctg | aac | tcc | agt | gat | atc | cac | 1469 |

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197 Phe Leu Gly Phe Val Val Glu Gln His Leu Asn Ser Ser Asp Ile His
198      425      430      435
200 cac att aat gaa atc aaa agg cag aac cag tcc ctt gtg tat ggc aaa 1517
201 His Ile Asn Glu Ile Lys Arg Gln Asn Gln Ser Leu Val Tyr Gly Lys
202      440      445      450
204 gtg gat agc ttc tgg aag aat aag aag atc tac ttg gac att att cac 1565
205 Val Asp Ser Phe Trp Lys Asn Lys Lys Ile Tyr Leu Asp Ile Ile His
206 455      460      465      470
208 aca tac atg gaa gtg cat gca act gtt tat ggc tcc agc aca aag aat 1613
209 Thr Tyr Met Glu Val His Ala Thr Val Tyr Gly Ser Ser Thr Lys Asn
210      475      480      485
212 att ccc agt tac gtg aaa aac cat ggt atc ctc agt gga cgg gac ctg 1661
213 Ile Pro Ser Tyr Val Lys Asn His Gly Ile Leu Ser Gly Arg Asp Leu
214      490      495      500
216 cag ttc ctt ctt cga gaa acc aag ttg ttt gtt gga ctt ggg ttc cct 1709
217 Gln Phe Leu Leu Arg Glu Thr Lys Leu Phe Val Gly Leu Gly Phe Pro
218      505      510      515
220 tac gag ggc cca gct ccc ctg gaa gct atc gca aat gga tgt gct ttt 1757
221 Tyr Glu Gly Pro Ala Pro Leu Glu Ala Ile Ala Asn Gly Cys Ala Phe
222      520      525      530
224 ctg aat ccc aag ttc aac cca ccc aaa agc agc aaa aac aca gac ttt 1805
225 Leu Asn Pro Lys Phe Asn Pro Pro Lys Ser Ser Lys Asn Thr Asp Phe
226 535      540      545      550
228 ttc att ggc aag cca act ctg aga gag ctg aca tcc cag cat cct tac 1853
229 Phe Ile Gly Lys Pro Thr Leu Arg Glu Leu Thr Ser Gln His Pro Tyr
230      555      560      565
232 gct gaa gtt ttc atc ggg cgg cca cat gtg tgg act gtt gac ctc aac 1901
233 Ala Glu Val Phe Ile Gly Arg Pro His Val Trp Thr Val Asp Leu Asn
234      570      575      580
236 aat cag gag gaa gta gag gat gca gtg aaa gca att tta aat cag aag 1949
237 Asn Gln Glu Glu Val Glu Asp Ala Val Lys Ala Ile Leu Asn Gln Lys
238      585      590      595
240 att gag cca tac atg cca tat gaa ttt acg tgc gag ggg atg cta cag 1997
241 Ile Glu Pro Tyr Met Pro Tyr Glu Phe Thr Cys Glu Gly Met Leu Gln
242      600      605      610
244 aga atc aat gct ttc att gaa aaa cag gac ttc tgc cat ggg caa gtg 2045
245 Arg Ile Asn Ala Phe Ile Glu Lys Gln Asp Phe Cys His Gly Gln Val
246 615      620      625      630
248 atg tgg cca ccc ctc agc gcc cta cag gtc aag ctt gct gag ccc ggg 2093
249 Met Trp Pro Pro Leu Ser Ala Leu Gln Val Lys Leu Ala Glu Pro Gly
250      635      640      645
252 cc 2095
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 16
256 <212> TYPE: PRT
257 <213> ORGANISM: Homo sapiens
259 <400> SEQUENCE: 7
260 Lys Ser Leu Ala Glu Lys Gln Asn Leu Glu Lys Arg Lys Arg Lys Lys
261 1 5 10 15

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264 <210> SEQ ID NO: 8
265 <211> LENGTH: 24
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: compound suppressing expression
272 <400> SEQUENCE: 8
273 gggagtgagg atgatgtagg gaag 24
275 <210> SEQ ID NO: 9
276 <211> LENGTH: 24
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: compound suppressing expression
283 <400> SEQUENCE: 9
284 atggggcaga ggaacttacg ttat 24
286 <210> SEQ ID NO: 10
287 <211> LENGTH: 6
288 <212> TYPE: PRT
289 <213> ORGANISM: Homo sapiens
291 <400> SEQUENCE: 10
292 Gly Arg Gly Lys Arg Arg
293 1 5
296 <210> SEQ ID NO: 11
297 <211> LENGTH: 6
298 <212> TYPE: PRT
299 <213> ORGANISM: Homo sapiens
301 <400> SEQUENCE: 11
302 Lys Arg Lys Arg Lys Lys
303 1 5
306 <210> SEQ ID NO: 12
307 <211> LENGTH: 6
308 <212> TYPE: PRT
309 <213> ORGANISM: Homo sapiens
311 <400> SEQUENCE: 12
312 Phe Ser Gly Gly Pro Leu
313 1 5
316 <210> SEQ ID NO: 13
317 <211> LENGTH: 5
318 <212> TYPE: PRT
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 13
322 His Phe Thr Ile Gln
323 1 5

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VERIFICATION SUMMARY

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